

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.71318 Seconds

(Without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613B-15

Perfect score: 602

Sequence: 1 QMATEFOOKHIINTPICNT.....ICVKNQYVPHFAGIGRCP 110

Scoring table: BLOSUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591.5	98.3	111	1	RNPO_RANCA
2	455	75.6	111	1	IECS_RANCA
3	374	62.1	111	1	RNPE_RANCA
4	277.5	46.1	104	1	RN30_RANPI
5	154.5	25.7	145	1	ANG3_MOUSE
6	149.5	24.8	145	1	ANGR_MOUSE
7	135.5	22.5	124	1	RNP_BALAC
8	135.5	22.5	145	1	ANGI_MOUSE
9	133.5	22.2	167	1	RNBR_BOVIN
10	132.5	22.0	124	1	RNP_PIG
11	131.5	21.8	119	1	RNP_IGUG
12	128.5	21.3	151	1	RNBR_CARCA
13	127.5	21.2	123	1	ANG2_BOVIN
14	127.5	21.2	141	1	RNBR_GIRCA
15	127.5	21.2	151	1	RNBR_AXIPR
16	125	20.8	146	1	ANGI_SAISC
17	124	20.6	146	1	ANGI_MIOA
18	123.5	20.5	143	1	RNBR_SHEEP
19	122.5	20.3	124	1	RNP_ANTMA
20	122.5	20.3	146	1	ANGI_CERAE
21	122	20.3	122	1	RNP_MACRO
22	120.5	20.0	128	1	RNP_MYOCO
23	120.5	20.0	149	1	RNP_MOUSE
24	120	19.9	146	1	ANGI_AOTR
25	120	19.9	147	1	ANGI_PONPY
26	119.5	19.9	123	1	ANGI_PIG
27	118.5	19.6	146	1	RNPE_CAVPO
28	118	19.5	128	1	ANGI_SAGOE
29	117.5	19.5	128	1	RNP_HORSE
30	116.5	19.4	124	1	RNP_CAMDR
31	116.5	19.4	128	1	RNP_PROCU
32	115.5	19.2	146	1	ANGI_MACMU
33	114	18.9	148	1	ANGI_BOVIN

34	113.5	18.9	124	1	RNP_RANTA	P00666 rangifer ta
35	113.5	18.9	146	1	ANGI_PAPHA	Q8wn64 papio hamad
36	113	18.8	147	1	ANGI_HUMAN	P03950 homo sapien
37	113	18.8	147	1	ANGI_PANTR	Q8me86 pan troglod
38	112.5	18.7	124	1	RNP_CARCA	P00664 capreolus c
39	112.5	18.7	148	1	RNLA_GIRCA	Q9jjh1 giraffa cam
40	112.5	18.7	148	1	RNLA_MOUSE	Q9jjh1 mus musculu
41	112	18.6	125	1	RNLA_RABIT	P24717 oryctolagus
42	111.5	18.5	130	1	RNP_CRITO	P24717 cricetus
43	111.5	18.5	147	1	RNLA_RAT	O55004 rattus norv
44	111.5	18.5	149	1	RNP_ACOCA	Q9wts1 acomys cahi
45	110.5	18.4	124	1	RNP_AEPME	P07847 aepyceos m

## ALIGNMENTS

RESULT 1	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	PI1916:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).			
OS	Rana catesbeiana (Bull. frog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.			
OX	NCBI_Taxid=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
RX	MEDLINE=87299649; PubMed=3304421;			
RA	Tilani K., Takio K., Kwada M., Nitta K., Sakakibara F., Kawachi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";			
RL	Biochemistry 26:2189-2194(1987).			
RN	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H.,			
RA	Takayanagi Y., Hakomori S., Tilani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=96437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTIN IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.			
CC	-1- SUBUNIT: MONOMER.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PIR: A27121; A27121.			

PDB: 1BC4; 28-OCT-98.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 DR Hydrolase: Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.  
 KW MOD\_RES 1  
 FT ACT\_SITE 10 10 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECFA CRC64;

Query Match 98.3%; Score 591.5; DB 1; Length 111;  
 Best Local Similarity 99.1%; Pred. No. 4.2e-57;  
 Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 QNMATFOOKHINPPII-CNTIMDNNNIYVGGCKRVNFTFISSATTVKATCTGVINNV 59  
 DB 1 QNMATFOOKHINPPII-CNTIMDNNNIYVGGCKRVNFTFISSATTVKATCTGVINNV 60

OY 60 LSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110  
 DB 61 LSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 111

RESULT 2  
 LECS\_RANCA STANDARD; PRT; 111 AA.  
 AC P18839;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-)  
 OS Rana japonica (Japanese reddish frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8402;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Egg;  
 RX MEDLINE=9103319; PubMed=2229005;  
 RA Kaniya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,  
 RT Takayana Y., Tani K.;  
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs."  
 RL J. Biochem. 108:139-143(1990).  
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE  
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN  
 CC REPRESENTS A LARGE VARIETY OF TUMOR CELLS, BUT IT  
 CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT ACT\_SITE 10 10 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 103 103 BY SIMILARITY.  
 FT DISULFID 19 72 BY SIMILARITY.  
 FT DISULFID 34 82  
 FT DISULFID 52 97

FT DISULFID 94 111  
 SQ SEQUENCE 111 AA; 12326 MW; FEEDBDF3834ED679 CRC64;

Query Match 75.6%; Score 455; DB 1; Length 111;  
 Best Local Similarity 78.4%; Pred. No. 2.2e-42;  
 Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

OY 1 QNMATFOOKHINPPII-CNTIMDNNNIYVGGCKRVNFTFISSATTVKATCTGVINNV 58  
 DB 1 QNMATFOOKHINPPII-CNTIMDNNNIYVGGCKRVNFTFISSATTVKATCTGVINNV 60

OY 59 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 DB 61 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 111

RESULT 3  
 RNPL\_RANCA STANDARD; PRT; 111 AA.  
 ID RNPL\_RANCA  
 AC P14626;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90130374; PubMed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RT Okazaki T., Ohgi K., Irie M.;  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver."  
 RL J. Biochem. 106:729-735(1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0085; JX0085.  
 DR HSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolase; Nuclease; Endonuclease.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10 10 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 104 104 BY SIMILARITY.  
 FT DISULFID 19 72 BY SIMILARITY.  
 FT DISULFID 34 82 BY SIMILARITY.  
 FT DISULFID 52 97 BY SIMILARITY.  
 FT DISULFID 94 111 PROBABLE.  
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 62.1%; Score 374; DB 1; Length 111;  
 Best Local Similarity 65.8%; Pred. No. 1.2e-33;  
 Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

OY 1 QNMATFOOKHINPPII-CNTIMDNNNIYVGGCKRVNFTFISSATTVKATCTGVINNV 58  
 DB 1 QNMATFOOKHINPPII-CNTIMDNNNIYVGGCKRVNFTFISSATTVKATCTGVINNV 60

OY 59 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 DB 61 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 111

RESULT 4  
 RN30\_RANPI STANDARD: PRT: 104 AA.  
 AC P22069;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE P-30 protein (EC 3.1.27.-) (onconase).  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RC SEQUENCE.  
 RP TISSUE=Embryo;  
 RX MEDLINE=91093131; PubMed=1985696;  
 RA Ardelt W., Mikulski S.M., Shogen K.;  
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";  
 RL J. Biol. Chem. 266:245-251(1991).  
 RN [2]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=93066156; PubMed=1438177;  
 RA Mosmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K., James M.N.G.;  
 RT "Comparative molecular modeling and crystallization of P-30 protein: a novel anti-tumor protein of Rana pipiens oocytes and early embryos.";  
 RL Proteins 14:392-400(1992).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=94166079; PubMed=8120892;  
 RA Mosmann S.C., Ardelt W., James M.N.G.;  
 RT "Refined 1.7 A x-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";  
 RL J. Mol. Biol. 236:1141-1153(1994).  
 CC -1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.  
 CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PDB: 1ONC; 31-JAN-94.  
 DR InterPro: IPR001427; RnaseA.  
 DR Pfam: PF00074; rnsaA; 1.  
 DR ProDom: PD000535; RnaseA; 1.  
 DR SMART: SM00052; Rnase\_Pc; 1.  
 DR PROSITE: PS00127; Rnase\_Pancreatic; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; 3D-structure.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10  
 FT ACT\_SITE 31  
 FT ACT\_SITE 97  
 FT DISULFID 19  
 FT DISULFID 30  
 FT DISULFID 75  
 FT DISULFID 87  
 FT DISULFID 104  
 FT HELIX 3  
 FT STRAND 10  
 FT STRAND 11  
 FT HELIX 12  
 FT HELIX 19  
 FT HELIX 22  
 FT TURN 23  
 FT TURN 24  
 FT TURN 26  
 FT STRAND 33  
 FT STRAND 38  
 FT STRAND 41  
 FT HELIX 48  
 FT TURN 49  
 FT TURN 50  
 FT STRAND 55  
 FT STRAND 58  
 FT TURN 63  
 FT TURN 70  
 FT TURN 74  
 FT STRAND 77  
 FT STRAND 84  
 FT TURN 86  
 FT TURN 91  
 FT TURN 92  
 FT TURN 93  
 FT STRAND 94  
 FT STRAND 101  
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2P9E56B4 CRC64;

Query Match 46.1%; Score 277.5; DB 1; Length 104;  
 Best Local Similarity 49.5%; Pred. No. 2, 9e-23;  
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 QNMATFOQKHIIINT-PIICNTIMDNNTIYVGGCKRVNTEFISSATVKAICGV1-NMN 58  
 DB 1 QDMVTFQKHIIITRDVDCONIMSTNLF----HCKDKNTFYSPREPKAICGIIASKN 56  
 QY 59 VLSTTRQLNTCTRTSTTPRCPSTSTETNIVCYKCKENQPVHPAIGRC 109  
 DB 57 VLTTSEFLSDC--NVTSRPCKYKIKSTNRCVCTCENQAPVHFGVGC 104  
 RESULT 5  
 ANG3\_MOUSE STANDARD: PRT: 145 AA.  
 AC P97802;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2) (EF-5).  
 DE ANG3 OR ANGL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=97184476; PubMed=9032278;  
 RA Fu X., Kamps M.P.;  
 RT "Ezra-Pbx1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 fibroblasts.";  
 RL Mol. Cell. Biol. 17:1503-1512(1997).  
 CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL: U72672; AAC05794.1;  
 DR HSSP: P10152; IAGL.  
 DR MGD: MGI:1201793; Angl.  
 DR InterPro: IPR001427; RnaseA.  
 DR Pfam: PF00074; rnsaA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RnaseA; 1.  
 DR SMART: SM00092; Rnase\_Pc; 1.  
 DR PROSITE: PS00127; Rnase\_Pancreatic; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis; Protein synthesis inhibitor; Signal.  
 FT SIGNAL 1  
 FT CHAIN 24  
 FT MOD\_RES 25  
 FT ACT\_SITE 37  
 FT ACT\_SITE 64  
 FT ACT\_SITE 137  
 FT DISULFID 50  
 FT DISULFID 63  
 FT DISULFID 81  
 FT DISULFID 130  
 SQ SEQUENCE 145 AA; 16696 MW; DE9D3BC92F1D682C CRC64;

```

Query Match      25.7%: Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%: Pred. No. 7,5e-10;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;

OY 33 CKRVNFTFISSATVKAIC-----TGVINNVLTSTRPOLNCTRTSITPR-PCPYSSRTE 85
    ||||| : ||| | : | : | : ||| : ||| | | : | :
DB 63 KEVNTFIDHDKNNIKAIKCGNGRPGV-NPRI-SNSRFQYTTCCHKGSPRPCCYNANF 120
    : || : || : ||| : ||| |
OY 86 TETNYICKVCENQVPVF 103
    : || : || : ||| : ||| |
DB 121 KDFRIIVLACEDGMPEVHF 138

RESULT 6.
ID ANGR_MOUSE STANDARD; PRT; 145 AA.
AC O64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
XX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RL protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U25159; AAA91367.1; -.
DR HSBP; P03950; IAAy.
DR MGD; MGI:104984; Angrp.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 22A6EB814429C4AD CXC64;

Query Match      24.8%; Score 149.5; DB 1; Length 145;
Best Local Similarity 43.4%; Pred. No. 2,6e-09;
Matches 33; Conservative 10; Mismatches 28; Indels 5; Gaps 3;

OY 33 CKRVNFTFISSATVKAIC---TGVINNV-LSTTRPOLNCTRTSITPR-PCPYSSRTE 87
    ||||| | : ||| | : | : | : ||| : ||| | | : | :
DB 63 CKDVNTFIDHTKNNIKAIKCGKGSPPYGRNLNLSKSRFCVTTCJTHKGRSPRPCCYRASKG 122

```

OY		88	TNYICVKNCENOYPVHF	103
		:     :		
Db		123	FRTIIGCNGMPVHF	138

RESULT 7  
RNP\_BALAC

ID	RNP_BALAC	STANDARD:	PRT:	124 AA.
AC	P00673:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).			
GN	RNASE1 OR RNS1.			
OS	Balaenoptera acutorostrata (Minke whale) (lesser rorqual).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Cetartiodactyla; Cetacea; Mysticeti;			
OX	Balaenopteridae; Balaenoptera.			
RN	NCR1_TaxID=9767;			
RP	[1]			
SEQUENCE:				
RP	MEDLINE=76277855; PubMed=962870;			
RX	Emmens M., Welling G.W., Beintema J.J.;			
RA	"The amino acid sequence of pike-whale (lessor-rorqual) pancreatic			
RT	ribonuclease.";			
RL	Biochem. J. 157:317-323(1976).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3' phosphate intermediates ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: PANCREAS.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PIR: A00818; NRMK.			
DR	HSSP: P00656; ISRN.			
DR	InterPro: IPR001427; RNaseA.			
DR	PIfam: PF00074; RNaseA; 1.			
DR	PRINTS: PR00794; RIBONUCLEASE.			
DR	PRODOM: PD000535; RNaseA; 1.			
DR	SMART: SMO0092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
FT	DISULFID 26 84			
FT	DISULFID 40 95			
FT	DISULFID 58 110			
FT	DISULFID 65 72			
FT	ACT_SITE 12 12			
FT	ACT_SITE 41 41			
FT	ACT_SITE 119 119			
FT	CARBOND 76 76			
SQ	SEQUENCE 124 AA; 14125 MW; F57475459F657E2D CRC64; MOLCULES. . . .); IN 30% OF THE			

Query Match 22.5%; Score 135.5; DB 1; Length 124;  
Best Local Similarity 33.3%; Pred. No. 7.le-08;  
Matches . 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

OY	6 FOQHII-----TPPICNTIMDNNIYYVGCKRYNTEFIISATTVKAICTGVIMNV 59     :   DB 8 FORGHDSGNSFGNNPNVCNMMMRR-KMDGGKRKPVTGRHELEDDVKAVCS---QKNV 63  OY 60 L-----STRFDLNTCTRTSTTRP-CPYSSRTETNYICVKE-NQY-PVHF 103   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   DB 64 LCKNGRFNCESNSTMIHTDCROTGSKYPCAYKKTQSKEKHILLACEGANPVVPHF 120
----	--

RESULT 8  
ANGI\_MOUSE

ID	ANGI_MOUSE	STANDARD:	PRT:	145 AA.
AC	P21570:			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			

```
Db      123 FRHVIVACENGLPVHF 138

RESULT_9
FNBR_BOVIN          STANDARD;       PRT;    167 AA.
ID FNBR_BOVIN          STANARND;       PRT;    167 AA.
AC P39873:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRN).
GN BRN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92093604; Pubmed=1754384;
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA Viola M., Palmeri M., Russo E., Furia A.;
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT and its expression in different regions of the brain.";
RL Nucleic Acids Res. 19:6469-6474(1991).
[2]
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC TISSUE-BRAIN.
RX MEDLINE=89214015; Pubmed=3243767;
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bovine brain.";
RL J. Biochem. 104:939-945(1988).
[3]
RP SEQUENCE OF 27-167 FROM N.A.
RX MEDLINE=9613017; Pubmed=8587129;
RA Conratone E., Belmonta J.J., Sasso M.P., Carsana A., Palmeri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species".;
RL J. Mol. Evol. 41:850-858(1995).
-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as their content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.slb.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X59767; CAA42439.1; -.
DR EMBL; S81744; AAB36138.1; -.
DR PIR; S20066; S20066.
DR PIR; JX0056; JX0056.
DR HSSP; P00656; 2RNS.
DR GlycoSuiteDB; P39873; -.
DR InterPro; IPRO01427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEAS.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyse; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL              1        26
FT CHAIN               27       167     RIBONUCLEASE, BRAIN.
FT ACT_SITE            38         BY SIMILARITY.
FT ACT_SITE             67         BY SIMILARITY.
FT ACT_SITE           145         BY SIMILARITY.
FT DISULFID             52         BY SIMILARITY.
FT DISULFID             66         BY SIMILARITY.
FT DISULFID             84         BY SIMILARITY.
FT DISULFID             91         BY SIMILARITY.
```

FT	DISULEID	40	95
FT	DISULEID	58	110
FT	DISULEID	65	72
FT	ACT_SITE	12	12
FT	ACT_SITE	41	41
FT	ACT_SITE	119	119
FT	CARBOHYD	21	21
FT	CARBOHYD	34	34
FT	CARBOHYD	76	76
SQ	SEQUENCE	124 AA:	13804 MW; 0AC28CDEI4111845 CRC64;

  

Query Match	22.0%;	Score 132.5;	DB 1;	Length 124;
Best Local Similarity	31.6%;	Pred. No. 1.5e-07;		
Matches	36;	Conservative	19;	Mismatches 42; Indels 17; Gaps 6

  

OY	6 FQQKHII-----INPILICNTIMDNINIYVGQCKRVNTEFLISATTKAICTGV-INNN	58
Dd	8 FQRQHMDPDSSSSNSNYCNLMMSRR-NMTGCRCKRVTMEFVHESLADVQAGSCQINVNCK	66
OY	59 VLSTTRPLNT-----CTRTSITPRP-CPISSRIETNYICYKCENO--YPVHF	103
Dd	67 NGQNCYSNSTMIHTDCRGFGSSXPCAVKASEQKHIIIVACGNGPPVPVHF	120

	RESULT	11
RNP_IGUG		
ID	RNP_IGUG	STANDARD; PRT; 119 AA.
AC	P80287;	
DT	01-FEB-1994 (Rel. 28, Created)	
DT	01-FEB-1994 (Rel. 28, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).	
OS	Iguana iguana (Common Iguana).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.	
OX	NCBI_Taxid=8517;	
RN	[1]	
RP	SEQUENCE.	
RC	TISSUE=Pancreas;	
RX	MEDLINE=94139745; PubMed=8307028;	
RA	Zhao W., Beintema J.J., Hofsteenge J.;	
RT	"The amino acid sequence of Iguana (Iguana iguana) pancreatic	
RT	ribonuclease.";	
RL	Eur. J. Biochem. 219:641-646(1994).-	
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-	
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P	
CC	with 2',3'-cyclic phosphate intermediates.	
CC	-1- SUBCELLULAR LOCATION: Secreted.	
CC	-1- TISSUE SPECIFICITY: PANCREAS.	
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.	
DR	HSSP; P00656; LISO.	
DR	Interpro: IPRO01427; RNaseA.	
DR	Pfam: PF00074; rnasea; 1.	
DR	PRINTS; PR00794; RIBONUCLEASE.	
DR	ProDom; PD00535; RNaseA; 1.	
DR	SMART; SM00092; RNase_Pc; 1.	
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.	
KM	Hydrolase; Nuclease; Endonuclease.	
FT	MOD_RES	1
FT	DISULFID	25
FT	DISULFID	39
FT	ACT_SITE	57
FT	ACT_SITE	10
FT	ACT_SITE	40
FT	ACT_SITE	113
SQ	SEQUENCE	119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;
	Query Match	21.8%; Score 131.5; DB 1; Length 119;
	Best Local Similarity	30.4%; Pred. No. 1.8e-07;
	Matches 35; Conservative	16; Mismatches 51; Indels 13; Gaps 4;
Y	1 ONNATGCOOKH-----INTPLICTIMDNNNIYVGCGCKRWNTFIISATTVKAIC-- 51	

Db 1 QDWSFONKHIDPETSASNPAYCDLMQOR- NLNPTCKCTNTNTVHASPSEIOOVCS 59  
 OY 52 --TGVINMNTSTRTFOLNTCTRTST-PPCPYSSRTFTNYCVCCENQYPVHF 103  
 Db 60 GGTHYEDNLKXDSNEFDLTDCKNKGSTAPSSCKYNGTPTGKTRIRACENNQPVHF 114

## RESULT 12

NRNR\_CAPCA STANDARD; PRT; 151 AA.  
 AC P79351;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Capreolus capreolus (Roe deer).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
 OC Cervidae; Odocolleinae; Capreolus.  
 NCBI\_TaxID=9858;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=98278442; PubMed=9611269;  
 RA Beukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,  
 RA Beukelman J.J.;  
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants."  
 RL Gene 213:259-268(1998).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: Y11673; CAA72371.1;  
 CC HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KM Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
 FT ACT\_SITE 41 41  
 FT DISULFID 26 84  
 FT DISULFID 40 95  
 FT DISULFID 58 110  
 FT DISULFID 65 72  
 FT CARBOHYD 62 62  
 FT CARBOHYD 129 129  
 FT CARBOHYD 133 133  
 FT CARBOHYD 133 133  
 SQ SEQUENCE 151 AA; 16971 MW; 392D0E6302F006A6 CRC64;

Query Match 21.3%; Score 128.5; DB 1; Length 151;  
 Best Local Similarity 29.4%; Pred. No. 5e-07;  
 Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;

OY 4 AFTQQRHI-----INTPIICNTIMDNNTIYVGCGCKRVNTFTIISATYKAICGVINM 57  
 ID NRNR\_CAPCA STANDARD; PRT; 151 AA.  
 AC Q29542; Q29533;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97409980; PubMed=9266695;  
 RA Strydom D.J., Bond M.D., Vaillee B.L.;  
 RT "An angiogenic protein from bovine serum and milk -- purification and  
 RT primary structure of angiogenin-2."  
 RL Eur. J. Biochem. 247:535-544(1997).  
 CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.  
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KM Protein synthesis inhibitor; Glycoprotein.  
 FT ACT\_SITE 12 12  
 FT ACT\_SITE 39 39  
 FT ACT\_SITE 113 113  
 FT DISULFID 25 80  
 FT DISULFID 38 91  
 FT DISULFID 56 106  
 FT CARBOHYD 33 33  
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-JUN-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-2 (EC 3.1.27.-).  
 GN ANG2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 OX [1]  
 RN SEQUENCE.  
 RP TISSUE=Serum, and Milk;  
 RX MEDLINE=97409980; PubMed=9266695;  
 RA Strydom D.J., Bond M.D., Vaillee B.L.;  
 RT "An angiogenic protein from bovine serum and milk -- purification and  
 RT primary structure of angiogenin-2."  
 RL Eur. J. Biochem. 247:535-544(1997).  
 CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.  
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KM Protein synthesis inhibitor; Glycoprotein.  
 FT ACT\_SITE 12 12  
 FT ACT\_SITE 39 39  
 FT ACT\_SITE 113 113  
 FT DISULFID 25 80  
 FT DISULFID 38 91  
 FT DISULFID 56 106  
 FT CARBOHYD 33 33  
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 123;  
 Best Local Similarity 30.6%; Pred. No. 5.1e-07;  
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

OY 6 FQCKHIINTPI-----ICNTIMDNNTIYVGCGCKRVNTFTIISATYKAIC--TGIVINM 57  
 Db 8 FLAKHDPSTGTGDDRCNTMERR--NMTRPKQNTFTFHGNSDIRAVCDPRNGEPPR.65  
 OY 58 NVLSTR-FQNTCTRTSTTR-PCPYSSRTFTNYCVCCENQYPVH 102  
 Db 66 NGLIRSRSPQVYTCRRHSGSPRPPCRYRAFRANRVIVIRCFDOPFIH 113  
 RESULT 14  
 NRNR\_GIRCA STANDARD; PRT; 141 AA.  
 ID Q29542; Q29533;  
 AC Q29542; Q29533;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffidae;  
 OC Giraffidae; Giraffa.  
 NCBI\_TaxID=9894;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97409980; PubMed=9266695;  
 RA Strydom D.J., Bond M.D., Vaillee B.L.;  
 RT "An angiogenic protein from bovine serum and milk -- purification and  
 RT primary structure of angiogenin-2."  
 RL Eur. J. Biochem. 247:535-544(1997).  
 CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.  
 CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnasea; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KM Protein synthesis inhibitor; Glycoprotein.  
 FT ACT\_SITE 12 12  
 FT ACT\_SITE 39 39  
 FT ACT\_SITE 113 113  
 FT DISULFID 25 80  
 FT DISULFID 38 91  
 FT DISULFID 56 106  
 FT CARBOHYD 33 33  
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

```

OX NCBI_TaxID=57737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breudelman H.J., van der Munnik N., Kleineland R.G., Furia A.,
RA Beintema J.J.;
RA "secretory ribonuclease genes and pseudogenes in true runnants.";
RL Gene 212:255-268(1998).
CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation .
CC The European Bioinformatics Institute. There are no restrictions on its use by
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch)).
CC
DR EMBL: Y11670; CAA72368.1; -.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA. 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Fc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACCT_SITE 41
FT DISULFID 26
FT DISULFID 40
FT DISULFID 58
FT DISULFID 65
FT CARBOHD 62
FT CARBOHD 129
FT CARBOHD 133
SQ SEQUENCE 151 AA; 16819 MW; E95F3757EFC5B233 CMC64;
Query Match 21.2%; Score 127.5; DB 1; Length 151;
Best Local Similarity 30.6%; Pred. NO. 6.4e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;
OY 4 ATFOOKHL-----INPIICNTIMDNNIYIVGSOCKRVNTEFIISATVKAICTGVLM 57
Db 6 AKFRROHMDAGSSSGNSNCNMKKR-RHTHRCKCPVNTEFHVESLDSKAVCS---QK 61
OY 58 NVL-----STRPOLNTCIRTSTTPRP-CYSSRFETNYICVKE-NQY-PVHA 104
Db 62 NITKKNGPCNOCYSNSTMNITDCRETSSKYVPNCAYKTSOKOKYITVACEGNPYPVHF 121
OY 105 G 105
Db 122 G 122

```

Search completed: June 25, 2003, 14:50:05  
Job time : 5.71318 secs